

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Murphy, Patricia D.
Allen, Antonette C.
Alvares, Christopher P.
Critz, Brenda S.
Olson, Sheri J.
Schelter, Denise B.
Zeng, Bin
- (ii) TITLE OF INVENTION: A Sequence of the Human BRCA1 Gene
- (iii) NUMBER OF SEQUENCES: 78
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: ONCORMED
 - (B) STREET: 200 PERRY PARKWAY
 - (C) CITY: GAITHERSBURG
 - (D) STATE: MD
 - (E) COUNTRY: USA
 - (F) ZIP: 20877
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: to be assigned
 - (B) FILING DATE: herewith
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: R. THOMAS GALLEGOS
 - (B) REGISTRATION NUMBER: 32,692

(C) REFERENCE/DOCKET NUMBER: PA-0054

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 301-527-2051

(B) TELEFAX: 301-208-6997

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5711 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 17

(B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCTCGCTGA GACTTCCTGG ACCCCGCACC AGGCTGTGGG GTTTCTCAGA TAACTGGGCC	60
CCTGCGCTCA GGAGGCCTTC ACCCTCTGCT CTGGGTAAAG TTCATTGGAA CAGAAAGAAA	120
TGGATTTATC TGCTCTTCGC GTTGAAGAAG TACAAAATGT CATTAAATGCT ATGCAGAAAA	180
TCTTAGAGTG TCCCATCTGT CTGGAGTTGA TCAAGGAACC TGTCTCCACA AAGTGTGACC	240
ACATATTTTG CAAATTTTGC ATGCTGAAAC TTCTCAACCA GAAGAAAGGG CCTTCACAGT	300

GTCCTTTATG TAAGAATGAT ATAACCAAAA GGAGCCTACA AGAAAGTACG AGATTTAGTC	360
AACTTGTTGA AGAGCTATTG AAAATCATTG GTGCTTTTCA GCTTGACACA GGTTCGGAGT	420
ATGCAAACAG CTATAATTTT GCAAAAAAGG AAAATAACTC TCCTGAACAT CTAAAAGATG	480
AAGTTTCTAT CATCCAAAGT ATGGGCTACA GAAACCGTGC CAAAAGACTT CTACAGAGTG	540
AACCCGAAAA TCCTTCCTTG CAGGAAACCA GTCTCAGTGT CCAACTCTCT AACCTTGGAA	600
CTGTGAGAAC TCTGAGGACA AAGCAGCGGA TACAACCTCA AAAGACGTCT GTCTACATTG	660
AATTGGGATC TGATTCTTCT GAAGATACCG TTAATAAGGC AACTTATTGC AGTGTGGGAG	720
ATCAAGAATT GTTACAAATC ACCCCTCAAG GAACCAGGGA TGAAATCAGT TTGGATTCTG	780
CAAAAAAGGC TGCTTGTGAA TTTTCTGAGA CGGATGTAAC AAATACTGAA CATCATCAAC	840
CCAGTAATAA TGATTTGAAC ACCACTGAGA AGCGTGCAGC TGAGAGGCAT CCAGAAAAGT	900
ATCAGGGTAG TTCTGTTTCA AACTTGCATG TGGAGCCATG TGGCACAAAT ACTCATGCCA	960
GCTCATTACA GCATGAGAAC AGCAGTTTAT TACTCACTAA AGACAGAATG AATGTAGAAA	1020
AGGCTGAATT CTGTAATAAA AGCAAACAGC CTGGCTTAGC AAGGAGCCAA CATAACAGAT	1080
GGGCTGGAAG TAAGGAAACA TGTAATGATA GCGGACTCC CAGCACAGAA AAAAAGGTAG	1140
ATCTGAATGC TGATCCCCTG TGTGAGAGAA AAGAATGGAA TAAGCAGAAA CTGCCATGCT	1200
CAGAGAATCC TAGAGATACT GAAGATGTTT CTTGGATAAC ACTAAATAGC AGCATTGAGA	1260
AAGTTAATGA GTGGTTTTCC AGAAGTGATG AACTGTTAGG TTCTGATGAC TCACATGATG	1320
GGGAGTCTGA ATCAAATGCC AAAGTAGCTG ATGTATTGGA CGTTCTAAAT GAGGTAGATG	1380
AATATTCTGG TTCTTCAGAG AAAATAGACT TACTGGCCAG TGATCCTCAT GAGGCTTTAA	1440
TATGTAAAAG TGAAAGAGTT CACTCCAAAT CAGTAGAGAG TAATATTGAA GACAAAATAT	1500

TCAAGGTTTC	AAAGCGCCAG	TCATTTGCTC	TGTTTTCAAA	TCCAGGAAAT	GCAGAAGAGG	2760
AATGTGCAAC	ATTCTCTGCC	CACTCTGGGT	CCTTAAAGAA	ACAAAGTCCA	AAAGTCACTT	2820
TTGAATGTGA	ACAAAAGGAA	GAAAATCAAG	GAAAGAATGA	GTCTAATATC	AAGCCTGTAC	2880
AGACAGTTAA	TATCACTGCA	GGCTTTCCTG	TGGTTGGTCA	GAAAGATAAG	CCAGTTGATA	2940
ATGCCAAATG	TAGTATCAAA	GGAGGCTCTA	GGTTTTGTCT	ATCATCTCAG	TTCAGAGGCA	3000
ACGAAACTGG	ACTCATTACT	CCAAATAAAC	ATGGACTTTT	ACAAAACCCA	TATCGTATAC	3060
CACCACTTTT	TCCCATCAAG	TCATTTGTTA	AAACTAAATG	TAAGAAAAAT	CTGCTAGAGG	3120
AAAACTTTGA	GGAACATTCA	ATGTCACCTG	AAAGAGAAAT	GGGAAATGAG	AACATTCCAA	3180
GTACAGTGAG	CACAATTAGC	CGTAATAACA	TTAGAGAAAA	TGTTTTTAAA	GGAGCCAGCT	3240
CAAGCAATAT	TAATGAAGTA	GGTTCAGTA	CTAATGAAGT	GGGCTCCAGT	ATTAATGAAA	3300
TAGGTTCCAG	TGATGAAAAC	ATTCAAGCAG	AACTAGGTAG	AAACAGAGGG	CCAAAATTGA	3360
ATGCTATGCT	TAGATTAGGG	GTTTTGCAAC	CTGAGGTCTA	TAAACAAAGT	CTTCCTGGAA	3420
GTAATTGTAA	GCATCCTGAA	ATAAAAAAGC	AAGAATATGA	AGAAAGTAGT	CAGACTGTTA	3480
ATACAGATTT	CTCTCCATAT	CTGATTTTCA	ATAACTTAGA	ACAGCCTATG	GGAAGTAGTC	3540
ATGCATCTCA	GGTTTGTTCT	GAGACACCTG	ATGACCTGTT	AGATGATGGT	GAAATAAAGG	3600
AAGATACTAG	TTTTGCTGAA	AATGACATTA	AGGAAAGTTC	TGCTGTTTTT	AGCAAAAGCG	3660
TCCAGAGAGG	AGAGCTTAGC	AGGAGTCCTA	GCCCTTTCAC	CCATACACAT	TTGGCTCAGG	3720
GTTACCGAAG	AGGGGCCAAG	AAATTAGAGT	CCTCAGAAGA	GAACCTATCT	AGTGAGGATG	3780
AAGAGCTTCC	CTGCTTCCAA	CACTTGTTAT	TTGGTAAAGT	AAACAATATA	CCTTCTCAGT	3840
CTACTAGGCA	TAGCACCGTT	GCTACCGAGT	GTCTGTCTAA	GAACACAGAG	GAGAATTTAT	3900

TATCATTGAA	GAATAGCTTA	AATGACTGCA	GTAACCAGGT	AATATTGGCA	AAGGCATCTC	3960
AGGAACATCA	CCTTAGTGAG	GAAACAAAAT	GTTCTGCTAG	CTTGTTTTCT	TCACAGTGCA	4020
GTGAATTGGA	AGACTTGACT	GCAAATACAA	ACACCCAGGA	TCCTTTCTTG	ATTGGTTCTT	4080
CCAAACAAAT	GAGGCATCAG	TCTGAAAGCC	AGGGAGTTGG	TCTGAGTGAC	AAGGAATTGG	4140
TTTCAGATGA	TGAAGAAAGA	GGAACGGGCT	TGGAAGAAAA	TAATCAAGAA	GAGCAAAGCA	4200
TGGATTCAAA	CTTAGGTGAA	GCAGCATCTG	GGTGTGAGAG	TGAAACAAGC	GTCTCTGAAG	4260
ACTGCTCAGG	GCTATCCTCT	CAGAGTGACA	TTTAAACCAC	TCAGCAGAGG	GATACCATGC	4320
AACATAACCT	GATAAAGCTC	CAGCAGGAAA	TGGCTGAACT	AGAAGCTGTG	TTAGAACAGC	4380
ATGGGAGCCA	GCCTTCTAAC	AGCTACCCTT	CCATCATAAG	TGACTCCTCT	GCCCTTGAGG	4440
ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAAGCAGT	ATTAACCTCA	CAGAAAAGTA	4500
GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTTCTGC	TGACAAGTTT	GAGGTGTCTG	4560
CAGATAGTTC	TACCAGTAAA	AATAAAGAAC	CAGGAGTGGA	AAGGTCATCC	CCTTCTAAAT	4620
GCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAATAGAA	4680
ACTACCCATC	TCAAGAGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	4740
AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	4800
CCCCTTACCT	GGAATCTGGA	ATCAGCCTCT	TCTCTGATGA	CCCTGAATCT	GATCCTTCTG	4860
AAGACAGAGC	CCCAGAGTCA	GCTCGTGTTG	GCAACATACC	ATCTTCAACC	TCTGCATTGA	4920
AAGTTCCCCA	ATTGAAAGTT	GCAGAATCTG	CCCAGGGTCC	AGCTGCTGCT	CATACTACTG	4980
ATACTGCTGG	GTATAATGCA	ATGGAAGAAA	GTGTGAGCAG	GGAGAAGCCA	GAATTGACAG	5040
CTTCAACAGA	AAGGGTCAAC	AAAAGAATGT	CCATGGTGGT	GTCTGGCCTG	ACCCCAAGAG	5100

AATTTATGCT CGTGTACAAG TTTGCCAGAA AACACCACAT CACTTTAACT AATCTAATTA 5160
 CTGAAGAGAC TACTCATGTT GTTATGAAAA CAGATGCTGA GTTTGTGTGT GAACGGACAC 5220
 TGAAATATTT TCTAGGAATT GCGGGAGGAA AATGGGTAGT TAGCTATTTT TGGGTGACCC 5280
 AGTCTATTAA AGAAAGAAAA ATGCTGAATG AGCATGATTT TGAAGTCAGA GGAGATGTGG 5340
 TCAATGGAAG AAACCACCAA GGTCCAAAGC GAGCAAGAGA ATCCCAGGAC AGAAAGATCT 5400
 TCAGGGGGCT AGAAATCTGT TGCTATGGGC CCTTCACCAA CATGCCCACA GATCAACTGG 5460
 AATGGATGGT ACAGCTGTGT GGTGCTTCTG TGGTGAAGGA GCTTTCATCA TTCACCCTTG 5520
 GCACAGGTGT CCACCCAATT GTGGTTGTGC AGCCAGATGC CTGGACAGAG GACAATGGCT 5580
 TCCATGCAAT TGGGCAGATG TGTGAGGCAC CTGTGGTGAC CCGAGAGTGG GTGTTGGACA 5640
 GTGTAGCACT CTACCAGTGC CAGGAGCTGG ACACCTACCT GATACCCAG ATCCCCCACA 5700
 GCCACTACTG A 5711

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 17
- (B) MAP POSITION: 17q21

[illegible]

[illegible]

	835					840						845					
Glu Ser Glu Leu Asp Ala Gln Tyr Leu Gln Asn Thr Phe Lys Val Ser	850					855						860					
Lys Arg Gln Ser Phe Ala Leu Phe Ser Asn Pro Gly Asn Ala Glu Glu	865					870						875					880
Glu Cys Ala Thr Phe Ser Ala His Ser Gly Ser Leu Lys Lys Gln Ser					885					890							895
Pro Lys Val Thr Phe Glu Cys Glu Gln Lys Glu Glu Asn Gln Gly Lys					900					905					910		
Asn Glu Ser Asn Ile Lys Pro Val Gln Thr Val Asn Ile Thr Ala Gly					915					920					925		
Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys					930					935					940		
Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly					945							955					960
Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn					965					970							975
Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr					980					985							990
Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met					995					1000					1005		
Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser					1010					1015					1020		
Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser					1025					1030					1035		1040
Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser					1045					1050							1055

Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe
1285 1290 1295

Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr
1300 1305 1310

Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser
1315 1320 1325

Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp
1330 1335 1340

Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser
1345 1350 1355 1360

Met Asp Ser Asn Leu Gly Glu Ala Ala Ser Gly Cys Glu Ser Glu Thr
1365 1370 1375

Ser Val Ser Glu Asp Cys Ser Gly Leu Ser Ser Gln Ser Asp Ile Leu
1380 1385 1390

Thr Thr Gln Gln Arg Asp Thr Met Gln His Asn Leu Ile Lys Leu Gln
1395 1400 1405

Gln Glu Met Ala Glu Leu Glu Ala Val Leu Glu Gln His Gly Ser Gln
1410 1415 1420

Pro Ser Asn Ser Tyr Pro Ser Ile Ile Ser Asp Ser Ser Ala Leu Glu
1425 1430 1435 1440

Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr
1445 1450 1455

Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu
1460 1465 1470

Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn
1475 1480 1485

Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu
1490. 1495 1500

Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg
1505 1510 1515 1520

Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu
1525 1530 1535

Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr
1540 1545 1550

Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile
1555 1560 1565

Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala
1570 1575 1580

Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu
1585 1590 1595 1600

Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala
1605 1610 1615

Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val
1620 1625 1630

Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys
1635 1640 1645

Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu
1650 1655 1660

Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile
1665 1670 1675 1680

Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val
1685 1690 1695

Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp
1700 1705 1710

Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met
1715 1720 1725

Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg
1730 1735 1740

Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile
1745 1750 1755 1760

Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro
1765 1770 1775

Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val
1780 1785 1790

Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val
1795 1800 1805

Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile
1810 1815 1820

Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp
1825 1830 1835 1840

Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro
1845 1850 1855

Gln Ile Pro His Ser His Tyr
1860

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

CAAAAAAGGC	TGCTTGTGAA	TTTTCTGAGA	CGGATGTAAC	AAATACTGAA	CATCATCAAC	840
CCAGTAATAA	TGATTTGAAC	ACCACTGAGA	AGCGTGCAGC	TGAGAGGCAT	CCAGAAAAGT	900
ATCAGGGTAG	TTCTGTTTCA	AACTTGCAATG	TGGAGCCATG	TGGCACAAAT	ACTCATGCCA	960
GCTCATTACA	GCATGAGAAC	AGCAGTTTAT	TACTCACTAA	AGACAGAATG	AATGTAGAAA	1020
AGGCTGAATT	CTGTAATAAA	AGCAAACAGC	CTGGCTTAGC	AAGGAGCCAA	CATAACAGAT	1080
GGGCTGGAAG	TAAGGAAACA	TGTAATGATA	GGCGGACTCC	CAGCACAGAA	AAAAAGGTAG	1140
ATCTGAATGC	TGATCCCCTG	TGTGAGAGAA	AAGAATGGAA	TAAGCAGAAA	CTGCCATGCT	1200
CAGAGAATCC	TAGAGATACT	GAAGATGTTT	CTTGGATAAC	ACTAAATAGC	AGCATTCAGA	1260
AAGTTAATGA	GTGGTTTTCC	AGAAGTGATG	AACTGTTAGG	TTCTGATGAC	TCACATGATG	1320
GGGAGTCTGA	ATCAAATGCC	AAAGTAGCTG	ATGTATTGGA	CGTTCTAAAT	GAGGTAGATG	1380
AATATTCTGG	TTCTTCAGAG	AAAATAGACT	TACTGGCCAG	TGATCCTCAT	GAGGCTTTAA	1440
TATGTAAAAG	TGAAAGAGTT	CACTCCAAAT	CAGTAGAGAG	TAATATTGAA	GACAAAATAT	1500
TTGGGAAAAC	CTATCGGAAG	AAGGCAAGCC	TCCCCAACTT	AAGCCATGTA	ACTGAAAATC	1560
TAATTATAGG	AGCATTTGTT	ACTGAGCCAC	AGATAATACA	AGAGCGTCCC	CTCACAAATA	1620
AATTAAAGCG	TAAAAGGAGA	CCTACATCAG	GCCTTCATCC	TGAGGATTTT	ATCAAGAAAG	1680
CAGATTTGGC	AGTTCAAAAG	ACTCCTGAAA	TGATAAATCA	GGGAACTAAC	CAAACGGAGC	1740
AGAATGGTCA	AGTGATGAAT	ATTACTAATA	GTGGTCATGA	GAATAAAACA	AAAGGTGATT	1800
CTATTTCAGAA	TGAGAAAAAT	CCTAACCCAA	TAGAATCACT	CGAAAAAGAA	TCTGCTTTCA	1860
AAACGAAAGC	TGAACCTATA	AGCAGCAGTA	TAAGCAATAT	GGAACCTCGAA	TTAAATATCC	1920
ACAATTCAAA	AGCACCTAAA	AAGAATAGGC	TGAGGAGGAA	GTCTTCTACC	AGGCATATTC	1980

ATGCGCTTGA	ACTAGTAGTC	AGTAGAAATC	TAAGCCACC	TAATTGTACT	GAATTGCAAA	206
TTGATAGTTG	TTCTAGCAGT	GAAGAGATAA	AGAAAAAAA	GTACAACCAA	ATGCCAGTCA	210
GGCACAGCAG	AAACCTACAA	CTCATGGAAG	GTAAAGAACC	TGCAACTGGA	GCCAAGAAGA	216
GTAACAAGCC	AAATGAACAG	ACAAGTAAAA	GACATGACAG	CGATACTTTC	CCAGAGCTGA	222
AGTTAACAAA	TGCACCTGGT	TCTTTTACTA	AGTGTTCAAA	TACCAGTGAA	CTTAAAGAAT	228
TTGTCAATCC	TAGCCTTCCA	AGAGAAGAAA	AAGAAGAGAA	ACTAGAAACA	GTTAAAGTGT	234
CTAATAATGC	TGAAGACCCC	AAAGATCTCA	TGTTAAGTGG	AGAAAGGGTT	TTGCAAACCTG	240
AAAGATCTGT	AGAGAGTAGC	AGTATTTTCAT	TGGTACCTGG	TACTGATTAT	GGCACTCAGG	246
AAAGTATCTC	GTTACTGGAA	GTTAGCACTC	TAGGGAAGGC	AAAAACAGAA	CCAAATAAAT	252
GTGTGAGTCA	GTGTGCAGCA	TTTGAAAACC	CCAAGGGACT	AATTCATGGT	TGTTCCAAAG	258
ATAATAGAAA	TGACACAGAA	GGCTTTAAGT	ATCCATTGGG	ACATGAAGTT	AACCACAGTC	264
GGGAAACAAG	CATAGAAATG	GAAGAAAGTG	AACTTGATGC	TCAGTATTTG	CAGAATACAT	270
TCAAGGTTTC	AAAGCGCCAG	TCATTTGCTC	TGTTTTCAAA	TCCAGGAAAT	GCAGAAGAGG	276
AATGTGCAAC	ATTCTCTGCC	CACTCTGGGT	CCTTAAAGAA	ACAAAGTCCA	AAAGTCACTT	282
TTGAATGTGA	ACAAAAGGAA	GAAAATCAAG	GAAAGAATGA	GTCTAATATC	AAGCCTGTAC	288
AGACAGTTAA	TATCACTGCA	GGCTTTCCTG	TGGTTGGTCA	GAAAGATAAG	CCAGTTGATA	294
ATGCCAAATG	TAGTATCAAA	GGAGGCTCTA	GGTTTTGTCT	ATCATCTCAG	TTCAGAGGCA	300
ACGAAACTGG	ACTCATTACT	CCAAATAAAC	ATGGACTTTT	ACAAAACCCA	TATCGTATAC	306
CACCACTTTT	TCCCATCAAG	TCATTTGTTA	AACTAAATG	TAAGAAAAAT	CTGCTAGAGG	312
AAAACCTTGA	GGAACATTCA	ATGTCACCTG	AAAGAGAAAT	GGGAAATGAG	AACATTCCAA	318

ATGGGAGCCA	GCCTTCTAAC	AGCTACCCTT	CCATCATAAG	TGACTCTTCT	GCCCTTGAGG	44
ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAAGCAGT	ATTAAGTTCA	CAGAAAAGTA	451
GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTTCTGC	TGACAAGTTT	GAGGTGTCTG	456
CAGATAGTTC	TACCAGTAAA	AATAAAGAAC	CAGGAGTGGA	AAGGTCATCC	CCTTCTAAAT	462
GCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAATAGAA	468
ACTACCCATC	TCAAGAGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	474
AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	4801
CCCCTTACCT	GGAATCTGGA	ATCAGCCTCT	TCTCTGATGA	CCCTGAATCT	GATCCTTCTG	4860
AAGACAGAGC	CCCAGAGTCA	GCTCGTGTTG	GCAACATACC	ATCTTCAACC	TCTGCATTGA	4920
AAGTTCCCCA	ATTGAAAGTT	GCAGAATCTG	CCCAGAGTCC	AGCTGCTGCT	CATACTACTG	4980
ATACTGCTGG	GTATAATGCA	ATGGAAGAAA	GTGTGAGCAG	GGAGAAGCCA	GAATTGACAG	5040
CTTCAACAGA	AAGGGTCAAC	AAAAGAATGT	CCATGGTGGT	GTCTGGCCTG	ACCCCAGAAG	5100
AATTTATGCT	CGTGTACAAG	TTTGCCAGAA	AACACCACAT	CACTTTAACT	AATCTAATTA	5160
CTGAAGAGAC	TACTCATGTT	GTTATGAAAA	CAGATGCTGA	GTTTGTGTGT	GAACGGACAC	5220
TGAAATATTT	TCTAGGAATT	GCGGGAGGAA	AATGGGTAGT	TAGCTATTTT	TGGGTGACCC	5280
AGTCTATTAA	AGAAAGAAAA	ATGCTGAATG	AGCATGATTT	TGAAGTCAGA	GGAGATGTGG	5340
TCAATGGAAG	AAACCACCAA	GGTCCAAAGC	GAGCAAGAGA	ATCCCAGGAC	AGAAAGATCT	5400
TCAGGGGGCT	AGAAATCTGT	TGCTATGGGC	CCTTCACCAA	CATGCCCACA	GATCAACTGG	5460
AATGGATGGT	ACAGCTGTGT	GGTGCTTCTG	TGGTGAAGGA	GCTTTCATCA	TTCACCCTTG	5520
GCACAGGTGT	CCACCCAATT	GTGGTTGTGC	AGCCAGATGC	CTGGACAGAG	GACAATGGCT	5580

TCCATGCAAT TGGGCAGATG TGTGAGGCAC CTGTGGTGAC CCGAGAGTGG GTGTTGGACA 5640
 GTGTAGCACT CTACCAAGTGC CAGGAGCTGG ACACCTACCT GATACCCCAG ATCCCCCACA 5700
 GCCACTACTG A 5711

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 17
- (B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Leu	Ser	Ala	Leu	Arg	Val	Glu	Glu	Val	Gln	Asn	Val	Ile	Asn
1					5				10					15	
Ala	Met	Gln	Lys	Ile	Leu	Glu	Cys	Pro	Ile	Cys	Leu	Glu	Leu	Ile	Lys
			20					25					30		
Glu	Pro	Val	Ser	Thr	Lys	Cys	Asp	His	Ile	Phe	Cys	Lys	Phe	Cys	Met
		35					40					45			
Leu	Lys	Leu	Leu	Asn	Gln	Lys	Lys	Gly	Pro	Ser	Gln	Cys	Pro	Leu	Cys
		50					55					60			

[illegible]

Pro	Cys	Gly	Thr	Asn	Thr	His	Ala	Ser	Ser	Leu	Gln	His	Glu	Asn	Ser
		275					280					285			

Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe
290 295 300

Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg
305 310 315 320

Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr
325 330 335

Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu
340 345 350

Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu
355 360 365

Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu
370 375 380

Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp
385 390 395 400

Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu
405 410 415

Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu
420 425 430

Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His
435 440 445

Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr
450 455 460

Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn
465 470 475 480

Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg

485	490	495
Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu		
500	505	510
His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr		
515	520	525
Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln		
530	535	540
Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp		
545	550	555
Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys		
565	570	575
Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser		
580	585	590
Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys		
595	600	605
Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu		
610	615	620
Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln		
625	630	635
Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn		
645	650	655
Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys		
660	665	670
Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr		
675	680	685
Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn		
690	695	700

Ala	Pro	Gly	Ser	Phe	Thr	Lys	Cys	Ser	Asn	Thr	Ser	Glu	Leu	Lys	Glu	705	710	715	720
Phe	Val	Asn	Pro	Ser	Leu	Pro	Arg	Glu	Glu	Lys	Glu	Glu	Lys	Leu	Glu	725	730	735	
Thr	Val	Lys	Val	Ser	Asn	Asn	Ala	Glu	Asp	Pro	Lys	Asp	Leu	Met	Leu	740	745	750	
Ser	Gly	Glu	Arg	Val	Leu	Gln	Thr	Glu	Arg	Ser	Val	Glu	Ser	Ser	Ser	755	760	765	
Ile	Ser	Leu	Val	Pro	Gly	Thr	Asp	Tyr	Gly	Thr	Gln	Glu	Ser	Ile	Ser	770	775	780	
Leu	Leu	Glu	Val	Ser	Thr	Leu	Gly	Lys	Ala	Lys	Thr	Glu	Pro	Asn	Lys	785	790	795	800
Cys	Val	Ser	Gln	Cys	Ala	Ala	Phe	Glu	Asn	Pro	Lys	Gly	Leu	Ile	His	805	810	815	
Gly	Cys	Ser	Lys	Asp	Asn	Arg	Asn	Asp	Thr	Glu	Gly	Phe	Lys	Tyr	Pro	820	825	830	
Leu	Gly	His	Glu	Val	Asn	His	Ser	Arg	Glu	Thr	Ser	Ile	Glu	Met	Glu	835	840	845	
Glu	Ser	Glu	Leu	Asp	Ala	Gln	Tyr	Leu	Gln	Asn	Thr	Phe	Lys	Val	Ser	850	855	860	
Lys	Arg	Gln	Ser	Phe	Ala	Leu	Phe	Ser	Asn	Pro	Gly	Asn	Ala	Glu	Glu	865	870	875	880
Glu	Cys	Ala	Thr	Phe	Ser	Ala	His	Ser	Gly	Ser	Leu	Lys	Lys	Gln	Ser	885	890	895	
Pro	Lys	Val	Thr	Phe	Glu	Cys	Glu	Gln	Lys	Glu	Glu	Asn	Gln	Gly	Lys	900	905	910	
Asn	Glu	Ser	Asn	Ile	Lys	Pro	Val	Gln	Thr	Val	Asn	Ile	Thr	Ala	Gly	915	920	925	

Phe Pro Val Val Gly Gln Lys Asp Lys Pro Val Asp Asn Ala Lys Cys
930 935 940

Ser Ile Lys Gly Gly Ser Arg Phe Cys Leu Ser Ser Gln Phe Arg Gly
945 950 955 960

Asn Glu Thr Gly Leu Ile Thr Pro Asn Lys His Gly Leu Leu Gln Asn
965 970 975

Pro Tyr Arg Ile Pro Pro Leu Phe Pro Ile Lys Ser Phe Val Lys Thr
980 985 990

Lys Cys Lys Lys Asn Leu Leu Glu Glu Asn Phe Glu Glu His Ser Met
995 1000 1005

Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser
1010 1015 1020

Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Glu Ala Ser
1025 1030 1035 1040

Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser
1045 1050 1055

Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu
1060 1065 1070

Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val
1075 1080 1085

Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys
1090 1095 1100

His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val
1105 1110 1115 1120

Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro
1125 1130 1135

Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp
1140 1145 1150

Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn
1155 1160 1165

Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Lys Gly
1170 1175 1180

Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln
1185 1190 1195 1200

Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu
1205 1210 1215

Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly
1220 1225 1230

Lys Val Asn Asn Ile Pro Ser Gln Ser Thr Arg His Ser Thr Val Ala
1235 1240 1245

Thr Glu Cys Leu Ser Lys Asn Thr Glu Glu Asn Leu Leu Ser Leu Lys
1250 1255 1260

Asn Ser Leu Asn Asp Cys Ser Asn Gln Val Ile Leu Ala Lys Ala Ser
1265 1270 1275 1280

Gln Glu His His Leu Ser Glu Glu Thr Lys Cys Ser Ala Ser Leu Phe
1285 1290 1295

Ser Ser Gln Cys Ser Glu Leu Glu Asp Leu Thr Ala Asn Thr Asn Thr
1300 1305 1310

Gln Asp Pro Phe Leu Ile Gly Ser Ser Lys Gln Met Arg His Gln Ser
1315 1320 1325

Glu Ser Gln Gly Val Gly Leu Ser Asp Lys Glu Leu Val Ser Asp Asp
1330 1335 1340

Glu Glu Arg Gly Thr Gly Leu Glu Glu Asn Asn Gln Glu Glu Gln Ser
1345 1350 1355 1360

1570	1575	1580
Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu		
1585	1590	1595 1600
Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Ser Pro Ala Ala		
1605	1610	1615
Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val		
1620	1625	1630
Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys		
1635	1640	1645
Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu		
1650	1655	1660
Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile		
1665	1670	1675 1680
Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val		
1685	1690	1695
Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp		
1700	1705	1710
Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met		
1715	1720	1725
Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg		
1730	1735	1740
Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile		
1745	1750	1755 1760
Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro		
1765	1770	1775
Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val		
1780	1785	1790

Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val
1795 1800 1805
Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile
1810 1815 1820
Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp
1825 1830 1835 1840
Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro
1845 1850 1855
Gln Ile Pro His Ser His Tyr
1860

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (B) STRAIN: BRCAL

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 17
- (B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

$$\begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \quad (a) \quad \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

CAGAGAATCC	TAGAGATACT	GAAGATG TTC	CTTGGATAAC	ACTAAATAGC	AGCATTCAGA	1260
AAGTTAATGA	GTGGTTTTCC	AGAAGTGATG	AACTGTTAGG	TTCTGATGAC	TCACATGATG	1320
GGGAGTCTGA	ATCAAATGCC	AAAGTAGCTG	ATGTATTGGA	CGTTCTAAAT	GAGGTAGATG	1380
AATATTCTGG	TTCTTCAGAG	AAAATAGACT	TACTGGCCAG	TGATCCTCAT	GAGGCTTTAA	1440
TATGTAAAAG	TGAAAGAGTT	CACTCCAAAT	CAGTAGAGAG	TAATATTGAA	GACAAAATAT	1500
TTGGGAAAAC	CTATCGGAAG	AAGGCAAGCC	TCCCCAACTT	AAGCCATGTA	ACTGAAAATC	1560
TAATTATAGG	AGCATTTGTT	ACTGAGCCAC	AGATAATACA	AGAGCGTCCC	CTCACAAATA	1620
AATTAAAGCG	TAAAAGGAGA	CCTACATCAG	GCCTTCATCC	TGAGGATTTT	ATCAAGAAAG	1680
CAGATTTGGC	AGTTCAAAAG	ACTCCTGAAA	TGATAAATCA	GGGAACTAAC	CAAACGGAGC	1740
AGAATGGTCA	AGTGATGAAT	ATTACTAATA	GTGGTCATGA	GAATAAAACA	AAAGGTGATT	1800
CTATTCAGAA	TGAGAAAAAT	CCTAACCCAA	TAGAATCACT	CGAAAAAGAA	TCTGCTTTCA	1860
AAACGAAAGC	TGAACCTATA	AGCAGCAGTA	TAAGCAATAT	GGAACCTCGAA	TTAAATATCC	1920
ACAATTCAAA	AGCACCTAAA	AAGAATAGGC	TGAGGAGGAA	GTCTTCTACC	AGGCATATTC	1980
ATGCGCTTGA	ACTAGTAGTC	AGTAGAAATC	TAAGCCCACC	TAATTGTACT	GAATTGCAAA	2040
TTGATAGTTG	TTCTAGCAGT	GAAGAGATAA	AGAAAAAATA	GTACAACCAA	ATGCCAGTCA	2100
GGCACAGCAG	AAACCTACAA	CTCATGGAAG	GTAAAGAACC	TGCAACTGGA	GCCAAGAAGA	2160
GTAACAAGCC	AAATGAACAG	ACAAGTAAAA	GACATGACAG	TGATACTTTC	CCAGAGCTGA	2220
AGTTAACAAA	TGCACCTGGT	TCTTTTACTA	AGTGTTCAAA	TACCAGTGAA	CTTAAAGAAT	2280
TTGTCAATCC	TAGCCTTCCA	AGAGAAGAAA	AAGAAGAGAA	ACTAGAAACA	GTAAAGTGT	2340
CTAATAATGC	TGAAGACCCC	AAAGATCTCA	TGTTAAGTGG	AGAAAGGGTT	TTGCAAAC TG	2400

AAAGATCTGT AGAGAGTAGC AGTATTTTAC TGGTACCTGG TACTGATTAT GGCACCTCAGG	2460
AAAGTATCTC GTTACTGGAA GTTAGCACTC TAGGGAAGGC AAAACAGAA CCAAATAAAT	2520
GTGTGAGTCA GTGTGCAGCA TTTGAAAACC CCAAGGGACT AATTCATGGT TGTTCCAAAG	2580
ATAATAGAAA TGACACAGAA GGCTTTAAGT ATCCATTGGG ACATGAAGTT AACCACAGTC	2640
GGGAAACAAG CATAGAAATG GAAGAAAGTG AACTTGATGC TCAGTATTTG CAGAATACAT	2700
TCAAGGTTTC AAAGCGCCAG TCATTTGCTC TGTTTTCAAA TCCAGGAAAT GCAGAAGAGG	2760
AATGTGCAAC ATTCTCTGCC CACTCTGGGT CCTTAAAGAA ACAAAGTCCA AAAGTCACTT	2820
TTGAATGTGA ACAAAGGAA GAAAATCAAG GAAAGAATGA GTCTAATATC AAGCCTGTAC	2880
AGACAGTTAA TATCACTGCA GGCTTTCCTG TGGTTGGTCA GAAAGATAAG CCAGTTGATA	2940
ATGCCAAATG TAGTATCAAA GGAGGCTCTA GGTTTTGTCT ATCATCTCAG TTCAGAGGCA	3000
ACGAAACTGG ACTCATTACT CCAAATAAAC ATGGACTTTT ACAAACCCA TATCGTATAC	3060
CACCACTTTT TCCCATCAAG TCATTTGTTA AAATAAATG TAAGAAAAAT CTGCTAGAGG	3120
AAACTTTTGA GGAACATTCA ATGTCACCTG AAAGAGAAAT GGGAAATGAG AACATTCCAA	3180
GTACAGTGAG CACAATTAGC CGTAATAACA TTAGAGAAAA TGTTTTTAAA GGAGCCAGCT	3240
CAAGCAATAT TAATGAAGTA GGTTCCAGTA CTAATGAAGT GGGCTCCAGT ATTAATGAAA	3300
TAGGTTCCAG TGATGAAAAC ATTCAAGCAG AACTAGGTAG AAACAGAGGG CCAAATTGA	3360
ATGCTATGCT TAGATTAGGG GTTTTGCAAC CTGAGGTCTA TAAACAAAGT CTTCTGGAA	3420
GTAATTGTAA GCATCCTGAA ATAAAAAGC AAGAATATGA AGAAGTAGTT CAGACTGTTA	3480
ATACAGATTT CTCTCCATAT CTGATTTTCTG ATAACTTAGA ACAGCCTATG GGAAGTAGTC	3540
ATGCATCTCA GGTGTGTCT GAGACACCTG ATGACCTGTT AGATGATGGT GAAATAAAGG	3600

AAGATACTAG	TTTTGCTGAA	AATGACATTA	AGGAAAGTTC	TGCTGTTTTT	AGCAAAAGCG	3660
TCCAGAGAGG	AGAGCTTAGC	AGGAGTCCTA	GCCCTTTCAC	CCATACACAT	TTGGCTCAGG	3720
GTTACCGAAG	AGGGGCCAAG	AAATTAGAGT	CCTCAGAAGA	GAAGTTATCT	AGTGAGGATG	3780
AAGAGCTTCC	CTGCTTCCAA	CACTTGTTAT	TTGGTAAAGT	AAACAATATA	CCTTCTCAGT	3840
CTACTAGGCA	TAGCACCGTT	GCTACCGAGT	GTCTGTCTAA	GAACACAGAG	GAGAATTTAT	3900
TATCATTGAA	GAATAGCTTA	AATGACTGCA	GTAACCAGGT	AATATTGGCA	AAGGCATCTC	3960
AGGAACATCA	CCTTAGTGAG	GAAACAAAAT	GTTCTGCTAG	CTTGTTTTCT	TCACAGTGCA	4020
GTGAATTGGA	AGACTTGACT	GCAAATACAA	ACACCCAGGA	TCCTTTCTTG	ATTGGTTCTT	4080
CCAAACAAAT	GAGGCATCAG	TCTGAAAGCC	AGGGAGTTGG	TCTGAGTGAC	AAGGAATTGG	4140
TTTCAGATGA	TGAAGAAAGA	GGAACGGGCT	TGGAAGAAAA	TAATCAAGAA	GAGCAAAGCA	4200
TGGATTCAAA	CTTAGGTGAA	GCAGCATCTG	GGTGTGAGAG	TGAAACAAGC	GTCTCTGAAG	4260
ACTGCTCAGG	GCTATCCTCT	CAGAGTGACA	TTTTAACCAC	TCAGCAGAGG	GATACCATGC	4320
AACATAACCT	GATAAAGCTC	CAGCAGGAAA	TGGCTGAACT	AGAAGCTGTG	TTAGAACAGC	4380
ATGGGAGCCA	GCCTTCTAAC	AGCTACCCTT	CCATCATAAG	TGACTCTTCT	GCCCTTGAGG	4440
ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAAGCAGT	ATTAAGTTCA	CAGAAAAGTA	4500
GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTTCTGC	TGACAAGTTT	GAGGTGTCTG	4560
CAGATAGTTC	TACCAGTAAA	AATAAAGAAC	CAGGAGTGGA	AAGGTCATCC	CCTTCTAAAT	4620
GCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAATAGAA	4680
ACTACCCATC	TCAAGAGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	4740
AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	4800

CCCCCTACCT	GGAATCTGGA	ATCAGCCTCT	TCTCTGATGA	CCCTGAATCT	GATCCTTCTG	4860
AAGACAGAGC	CCCAGAGTCA	GCTCGTGTTG	GCAACATACC	ATCTTCAACC	TCTGCATTGA	4920
AAGTTCCCCA	ATTGAAAGTT	GCAGAATCTG	CCCAGGGTCC	AGCTGCTGCT	CATACTACTG	4980
ATACTGCTGG	GTATAATGCA	ATGGAAGAAA	GTGTGAGCAG	GGAGAAGCCA	GAATTGACAG	5040
CTTCAACAGA	AAGGGTCAAC	AAAAGAATGT	CCATGGTGGT	GTCTGGCCTG	ACCCCAGAAG	5100
AATTTATGCT	CGTGTACAAG	TTTGCCAGAA	AACACCACAT	CACTTTAACT	AATCTAATTA	5160
CTGAAGAGAC	TACTCATGTT	GTTATGAAAA	CAGATGCTGA	GTTTGTGTGT	GAACGGACAC	5220
TGAAATATTT	TCTAGGAATT	GCGGGAGGAA	AATGGGTAGT	TAGCTATTTT	TGGGTGACCC	5280
AGTCTATTAA	AGAAAGAAAA	ATGCTGAATG	AGCATGATTT	TGAAGTCAGA	GGAGATGTGG	5340
TCAATGGAAG	AAACCACCAA	GGTCCAAAGC	GAGCAAGAGA	ATCCCAGGAC	AGAAAGATCT	5400
TCAGGGGGCT	AGAAATCTGT	TGCTATGGGC	CCTTCACCAA	CATGCCCACA	GATCAACTGG	5460
AATGGATGGT	ACAGCTGTGT	GGTGCTTCTG	TGGTGAAGGA	GCTTTCATCA	TTCACCCTTG	5520
GCACAGGTGT	CCACCCAATT	GTGGTTGTGC	AGCCAGATGC	CTGGACAGAG	GACAATGGCT	5580
TCCATGCAAT	TGGGCAGATG	TGTGAGGCAC	CTGTGGTGAC	CCGAGAGTGG	GTGTTGGACA	5640
GTGTAGCACT	CTACCAGTGC	CAGGAGCTGG	ACACCTACCT	GATACCCCAG	ATCCCCCACA	5700
GCCACTACTG	A					5711

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1863 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

Pro Ser Leu Gln Glu Thr Ser Leu Ser-Val Gln Leu Ser Asn Leu Gly
145 150 155 160

Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
165 170 175

Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
180 185 190

Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
195 200 205

Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala
210 215 220

Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln
225 230 235 240

Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg
245 250 255

His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu
260 265 270

Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser
275 280 285

Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe
290 295 300

Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg
305 310 315 320

Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr
325 330 335

Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu
340 345 350

Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu
 355 360 365
 Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu
 370 375 380
 Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp
 385 390 395 400
 Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu
 405 410 415
 Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu
 420 425 430
 Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His
 435 440 445
 Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr
 450 455 460
 Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn
 465 470 475 480
 Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg
 485 490 495
 Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu
 500 505 510
 His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr
 515 520 525
 Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln
 530 535 540
 Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp
 545 550 555 560
 Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys

565	570	575
Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser		
580	585	590
Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys		
595	600	605
Asn Arg Leu Arg Arg Lys Ser Ser Thr Arg His Ile His Ala Leu Glu		
610	615	620
Leu Val Val Ser Arg Asn Leu Ser Pro Pro Asn Cys Thr Glu Leu Gln		
625	630	635
Ile Asp Ser Cys Ser Ser Ser Glu Glu Ile Lys Lys Lys Lys Tyr Asn		
645	650	655
Gln Met Pro Val Arg His Ser Arg Asn Leu Gln Leu Met Glu Gly Lys		
660	665	670
Glu Pro Ala Thr Gly Ala Lys Lys Ser Asn Lys Pro Asn Glu Gln Thr		
675	680	685
Ser Lys Arg His Asp Ser Asp Thr Phe Pro Glu Leu Lys Leu Thr Asn		
690	695	700
Ala Pro Gly Ser Phe Thr Lys Cys Ser Asn Thr Ser Glu Leu Lys Glu		
705	710	715
Phe Val Asn Pro Ser Leu Pro Arg Glu Glu Lys Glu Glu Lys Leu Glu		
725	730	735
Thr Val Lys Val Ser Asn Asn Ala Glu Asp Pro Lys Asp Leu Met Leu		
740	745	750
Ser Gly Glu Arg Val Leu Gln Thr Glu Arg Ser Val Glu Ser Ser Ser		
755	760	765
Ile Ser Leu Val Pro Gly Thr Asp Tyr Gly Thr Gln Glu Ser Ile Ser		
770	775	780

Ser Pro Glu Arg Glu Met Gly Asn Glu Asn Ile Pro Ser Thr Val Ser
1010 1015 1020

Thr Ile Ser Arg Asn Asn Ile Arg Glu Asn Val Phe Lys Gly Ala Ser
1025 1030 1035 1040

Ser Ser Asn Ile Asn Glu Val Gly Ser Ser Thr Asn Glu Val Gly Ser
1045 1050 1055

Ser Ile Asn Glu Ile Gly Ser Ser Asp Glu Asn Ile Gln Ala Glu Leu
1060 1065 1070

Gly Arg Asn Arg Gly Pro Lys Leu Asn Ala Met Leu Arg Leu Gly Val
1075 1080 1085

Leu Gln Pro Glu Val Tyr Lys Gln Ser Leu Pro Gly Ser Asn Cys Lys
1090 1095 1100

His Pro Glu Ile Lys Lys Gln Glu Tyr Glu Glu Val Val Gln Thr Val
1105 1110 1115 1120

Asn Thr Asp Phe Ser Pro Tyr Leu Ile Ser Asp Asn Leu Glu Gln Pro
1125 1130 1135

Met Gly Ser Ser His Ala Ser Gln Val Cys Ser Glu Thr Pro Asp Asp
1140 1145 1150

Leu Leu Asp Asp Gly Glu Ile Lys Glu Asp Thr Ser Phe Ala Glu Asn
1155 1160 1165

Asp Ile Lys Glu Ser Ser Ala Val Phe Ser Lys Ser Val Gln Arg Gly
1170 1175 1180

Glu Leu Ser Arg Ser Pro Ser Pro Phe Thr His Thr His Leu Ala Gln
1185 1190 1195 1200

Gly Tyr Arg Arg Gly Ala Lys Lys Leu Glu Ser Ser Glu Glu Asn Leu
1205 1210 1215

Ser Ser Glu Asp Glu Glu Leu Pro Cys Phe Gln His Leu Leu Phe Gly

!

[REDACTED]

Asp Leu Arg Asn Pro Glu Gln Ser Thr Ser Glu Lys Ala Val Leu Thr
1445 1450 1455

Ser Gln Lys Ser Ser Glu Tyr Pro Ile Ser Gln Asn Pro Glu Gly Leu
1460 1465 1470

Ser Ala Asp Lys Phe Glu Val Ser Ala Asp Ser Ser Thr Ser Lys Asn
1475 1480 1485

Lys Glu Pro Gly Val Glu Arg Ser Ser Pro Ser Lys Cys Pro Ser Leu
1490 1495 1500

Asp Asp Arg Trp Tyr Met His Ser Cys Ser Gly Ser Leu Gln Asn Arg
1505 1510 1515 1520

Asn Tyr Pro Ser Gln Glu Glu Leu Ile Lys Val Val Asp Val Glu Glu
1525 1530 1535

Gln Gln Leu Glu Glu Ser Gly Pro His Asp Leu Thr Glu Thr Ser Tyr
1540 1545 1550

Leu Pro Arg Gln Asp Leu Glu Gly Thr Pro Tyr Leu Glu Ser Gly Ile
1555 1560 1565

Ser Leu Phe Ser Asp Asp Pro Glu Ser Asp Pro Ser Glu Asp Arg Ala
1570 1575 1580

Pro Glu Ser Ala Arg Val Gly Asn Ile Pro Ser Ser Thr Ser Ala Leu
1585 1590 1595 1600

Lys Val Pro Gln Leu Lys Val Ala Glu Ser Ala Gln Gly Pro Ala Ala
1605 1610 1615

Ala His Thr Thr Asp Thr Ala Gly Tyr Asn Ala Met Glu Glu Ser Val
1620 1625 1630

Ser Arg Glu Lys Pro Glu Leu Thr Ala Ser Thr Glu Arg Val Asn Lys
1635 1640 1645

Arg Met Ser Met Val Val Ser Gly Leu Thr Pro Glu Glu Phe Met Leu
1650 1655 1660

Val Tyr Lys Phe Ala Arg Lys His His Ile Thr Leu Thr Asn Leu Ile
1665 1670 1675 1680

Thr Glu Glu Thr Thr His Val Val Met Lys Thr Asp Ala Glu Phe Val
1685 1690 1695

Cys Glu Arg Thr Leu Lys Tyr Phe Leu Gly Ile Ala Gly Gly Lys Trp
1700 1705 1710

Val Val Ser Tyr Phe Trp Val Thr Gln Ser Ile Lys Glu Arg Lys Met
1715 1720 1725

Leu Asn Glu His Asp Phe Glu Val Arg Gly Asp Val Val Asn Gly Arg
1730 1735 1740

Asn His Gln Gly Pro Lys Arg Ala Arg Glu Ser Gln Asp Arg Lys Ile
1745 1750 1755 1760

Phe Arg Gly Leu Glu Ile Cys Cys Tyr Gly Pro Phe Thr Asn Met Pro
1765 1770 1775

Thr Asp Gln Leu Glu Trp Met Val Gln Leu Cys Gly Ala Ser Val Val
1780 1785 1790

Lys Glu Leu Ser Ser Phe Thr Leu Gly Thr Gly Val His Pro Ile Val
1795 1800 1805

Val Val Gln Pro Asp Ala Trp Thr Glu Asp Asn Gly Phe His Ala Ile
1810 1815 1820

Gly Gln Met Cys Glu Ala Pro Val Val Thr Arg Glu Trp Val Leu Asp
1825 1830 1835 1840

Ser Val Ala Leu Tyr Gln Cys Gln Glu Leu Asp Thr Tyr Leu Ile Pro
1845 1850 1855

Gln Ile Pro His Ser His Tyr
1860



03075446322, 03075446322

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (B) STRAIN: 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGTTGTCA TTTTATAAAC CTTT

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (B) STRAIN: 2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTCTTTTCT TCCCTAGTAT GT

22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 3F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TCCTGACACA GCAGACATTT A

2:

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 3R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGGATTTTC GTTCTCACTT A

21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 5F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTCTTAAGGG CAGTTGTGAG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 5R-M13* primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCCTACTGT GGTTGCTTCC

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 6/7F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTATTTTAG TGTCTTAAA AGG

2

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 6R

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTCATGGAC AGCACTTGAG TG

22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 7F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CACAACAAAG AGCATACATA GGG

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 6/7R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCGGGTTTAC TCTGTAGAAG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 8F1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCTCTTCAG GAGGAAAAGC A

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 8R1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCTGCCTACC ACAAATACAA A

21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

[illegible]

(vi) ORIGINAL SOURCE:

(B) STRAIN: 10F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGTCAGCTT TCTGTAATCG

2.

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 10R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTATCTACCC ACTCTCTTCT TCAG

24

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCACCTCCAA GGTGTATCA

19

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTTATGTTG GCTCCTTGCT

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11BF1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CACTAAAGAC AGAATGAATC TA

22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11BR1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAAGAACCAG AATATTCATC TA

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11CF1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGATGGGGAG TCTGAATCAA

2

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (B) STRAIN: 11CR1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCTGCTTTCT TGATAAAATC CT

22

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 - (B) STRAIN: 11DF1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGCGTCCCCT CACAAATAAA

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11DR1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCAAGCGCAT GAATATGCCT

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTATAAGCAA TATGGAACTC GA

22

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

$\frac{1}{2} \left(\frac{1}{2} + \frac{1}{2} \right) = \frac{1}{2}$

- (A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTAAGTTCACT GGTATTTGAA CA

23

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGCGATA CTTTCCCAGA

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

$$\frac{1}{\sqrt{\pi}} \left(\frac{x_0 + i y_0}{r} \right)^n = \sum_{k=0}^{\infty} \frac{n!}{k!} \frac{(x_0 - i y_0)^k}{r^{k+1}} \quad (7)$$

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TGGAACAACC ATGAATTAGT C

21

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:.

(B) STRAIN: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAAGTTAGC ACTCTAGGGA

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11GR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCAGTGATAT TAACTGTCTG TA

22

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGGGTCCTTA AAGAAACAAA GT

22

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAGGTGACA TTGAATCTTC C

21

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCACTTTTTTC CCATCAAGTC A

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCAGGATGCT TACAATTACT TC

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAAAATTGAA TGCTATGCTT AGA

23

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 11JR primer

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11KF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11KR-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

[illegible]

TATTTGCAGT CAAGTCTTCC AA

22

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11LF-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTAATATTGG CAAAGGCATC. T

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAATGTGC TCCCCAAAAG CA

22

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AATGGAAAGC TTCTCAAAGT A

21

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATGTTGGAGC TAGGTCCTTA C

21

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: not relevant

(vi) ORIGINAL SOURCE:

(B) STRAIN: 15F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGGCTGCCCA GGAAGTATG

19

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 15R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AACCAGAATA TCTTTATGTA GGA

23

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 16F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AATTCTTAAC AGAGACCAGA AC

22

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 16R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAACTCTTT CCAGAATGTT GT

22

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 17F primer

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGTAGAACG TGCAGGATTG

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 17R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCGCCTCATG TGGTTTTA

18

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 18F primer

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGCTCTTTAG CTTCTTAGGA C

21

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 18R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAGACCATT TCCCAGCATC

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 19F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CTGTCATTCT TCCTGTGCTC

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGTAGAACG TGCAGGATTG

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 17R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

TCGCCTCATG TGGTTTTA

18

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (B) STRAIN: 18F primer

$\frac{1}{2} \left(\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & i \\ -1 & i \end{pmatrix} + \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & -i \\ 1 & i \end{pmatrix} \right) = \frac{1}{2} \begin{pmatrix} 2 & 0 \\ 0 & 2 \end{pmatrix} = I$

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

(2) INFORMATION FOR SEQ ID NO:65:

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

(2) INFORMATION FOR SEQ ID NO:66:

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 21R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTAGAGAAAT AGAATAGCCT CT

22

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 22F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TCCCATTGAG AGGTCTTGCT

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

[illegible]

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 22R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAGAAGACTT CTGAGGCTAC

20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 23F-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TGAAGTGACA GTTCCAGTAG T

21

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

[illegible]

(vi) ORIGINAL SOURCE:

(B) STRAIN: 23R-1 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATTTTAGCC ATTCATTCAA CAA

23

(2) INFORMATION FOR SEQ ID NO:71:-

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 24F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGAATTGAC ACTAATCTCT GC

22

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(B) STRAIN: 24R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTAGCCAGGA CAGTAGAAGG A

21